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Human papillomavirus (HPV) genotypes among HIV-infected and HIV-uninfected women in Mozambique

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Background

The objective of this study was to determine the prevalence of HPV infection and related genotypes in a group of HIV-infected women and in a control group of HIV-uninfected women. To our knowledge, it is the first study such study conducted in Mozambique.

Methods

The study was conducted in a public health center in Maputo. It was performed in the context of the Drug Resource Enhancement against AIDS and Malnutrition (DREAM) program, managed by the Community of Sant'Egidio within the national health system in collaboration with Ministry of Health. This is a prospective, two-arm, observational study. The first arm includes HIV- infected women while the second arm involves a control group of HIV-uninfected women. The enrollment period lasted 6 months (August 2007- January 2008). The observation period was 6 months. HPV detection genotyping was performed using CLINICAL ARRAYS® (GENOMICA SAU). HIV was detected with b-DNA assay (HIVç1 RNA 3.0, Bayer Health Care).

Results

The study involved 191 participants: 141 HIV-infected and 50 HIV-uninfected women. HPV was found in 126/141 (89.4%) of those HIV infected and in 33/50 (66%) of HIV-uninfected subjects ($p < 0.001$). In HIV-infected women there were 94/126 (74.6%) HPV-multiple-infections while in HIV-uninfected women there were 22/33 (66.6%) ($p = 0.375$). Twenty-nine distinct HPV types were identified among the 141 HIV-infected women, of which 16 viral types were classified as cancer high-risk or probable high-risk viruses. The most common types identified were HPV types 58 (12.1%, $p < 0.001$), 16 (10.7%, $p = 0.06$), 61 (8.4%, $p < 0.05$), 53 (7.9%, $p = 0.55$) and 6 (7.6%, $p = 0.41$). Nineteen distinct HPV genotypes were identified among the 50 HIV-uninfected women. Ten types were of high-risk or probable high-risk. The most common types identified in HIV-uninfected subjects were HPV types 53 (10.4%), 6 (9.1%), 16 (9.1%), 18 (9.1%) and 66 (7.8%).

Discussion

HPV infection was *mainly* associated with HIV positive status. HPV multiple infections were high in the population studied, independently of HIV status. HPV Genotypes are different in the two groups. The HPV types identified are partially different from those more commonly identified in Western countries.

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